

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/560,237
Source: IFWP
Date Processed by STIC: 4/27/07

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IFWP

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/560,237

DATE: 04/27/2007
TIME: 11:45:32

Input Set : A:\05081151.APP
Output Set: N:\CRF4\04272007\J560237.raw

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3 <110> APPLICANT: DUCOMMUN, BERNARD
4           MONSARRAT, BERNARD
5           PRIGENT, CLAUDE
7 <120> TITLE OF INVENTION: NOVEL PHOSPHORYLATED SEQUENCES OF CDC25B
PHOSPHATASE,
8           ANTIBODIES DIRECTED AGAINST THESE SEQUENCES AS WELL AS
9           THEIR USE
11 <130> FILE REFERENCE: 0508-1151
13 <140> CURRENT APPLICATION NUMBER: 10/560,237
14 <141> CURRENT FILING DATE: 2005-12-12
16 <150> PRIOR APPLICATION NUMBER: PCT/FR04/001416
17 <151> PRIOR FILING DATE: 2004-06-08
19 <150> PRIOR APPLICATION NUMBER: FR 0307095
20 <151> PRIOR FILING DATE: 2003-06-12
22 <160> NUMBER OF SEQ ID NOS: 11
24 <170> SOFTWARE: PatentIn Ver. 3.3
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 19
28 <212> TYPE: PRT
29 <213> ORGANISM: Homo sapiens
31 <220> FEATURE:
32 <221> NAME/KEY: MOD_RES
33 <222> LOCATION: (10)
34 <223> OTHER INFORMATION: PHOSPHORYLATION
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51 <222> LOCATION: (7)
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60 <211> LENGTH: 566
61 <212> TYPE: PRT
62 <213> ORGANISM: Homo sapiens
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65 <221> NAME/KEY: MOD_RES
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 67 <223> OTHER INFORMATION: PHOSPHORYLATION
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 73 Ala Gly Val Cys Gly Gly Ala Gln Arg Pro Gly His Leu Pro Gly Leu
 74 20 25 30
 76 Leu Leu Gly Ser His Gly Leu Leu Gly Ser Pro Val Arg Ala Ala Ala
 77 35 40 45
 79 Ser Ser Pro Val Thr Thr Leu Thr Gln Thr Met His Asp Leu Ala Gly
 80 50 55 60
 82 Leu Gly Ser Arg Ser Arg Leu Thr His Leu Ser Leu Ser Arg Arg Ala
 83 65 70 75 80
 85 Ser Glu Ser Ser Leu Ser Ser Glu Ser Ser Glu Ser Ser Asp Ala Gly
 86 85 90 95
 88 Leu Cys Met Asp Ser Pro Ser Pro Met Asp Pro His Met Ala Glu Gln
 89 100 105 110
 91 Thr Phe Glu Gln Ala Ile Gln Ala Ala Ser Arg Ile Ile Arg Asn Glu
 92 115 120 125
 94 Gln Phe Ala Ile Arg Arg Phe Gln Ser Met Pro Val Arg Leu Leu Gly
 95 130 135 140
 97 His Ser Pro Val Leu Arg Asn Ile Thr Asn Ser Gln Ala Pro Asp Gly
 98 145 150 155 160
 100 Arg Arg Lys Ser Glu Ala Gly Ser Gly Ala Ala Ser Ser Ser Gly Glu
 101 165 170 175
 103 Asp Lys Glu Asn Asp Gly Phe Val Phe Lys Met Pro Trp Lys Pro Thr
 104 180 185 190
 106 His Pro Ser Ser Thr His Ala Leu Ala Glu Trp Ala Ser Arg Arg Glu
 107 195 200 205
 109 Ala Phe Ala Gln Arg Pro Ser Ser Ala Pro Asp Leu Met Cys Leu Ser
 110 210 215 220
 112 Pro Asp Arg Lys Met Glu Val Glu Glu Leu Ser Pro Leu Ala Leu Gly
 113 225 230 235 240
 115 Arg Phe Ser Leu Thr Pro Ala Glu Gly Asp Thr Glu Glu Asp Asp Gly
 116 245 250 255
 118 Phe Val Asp Ile Leu Glu Ser Asp Leu Lys Asp Asp Asp Ala Val Pro
 119 260 265 270
 121 Pro Gly Met Glu Ser Leu Ile Ser Ala Pro Leu Val Lys Thr Leu Glu
 122 275 280 285
 124 Lys Glu Glu Glu Lys Asp Leu Val Met Tyr Ser Lys Cys Gln Arg Leu
 125 290 295 300
 127 Phe Arg Ser Pro Ser Met Pro Cys Ser Val Ile Arg Pro Ile Leu Lys
 128 305 310 315 320
 130 Arg Leu Glu Arg Pro Gln Asp Arg Asp Thr Pro Val Gln Asn Lys Arg
 131 325 330 335
 133 Arg Arg Ser Val Thr Pro Pro Glu Glu Gln Gln Glu Ala Glu Glu Pro
 134 340 345 350
 136 Lys Ala Arg Val Leu Arg Ser Lys Ser Leu Cys His Asp Glu Ile Glu

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137	355	360	365
139	Asn Leu Leu Asp Ser Asp His Arg Glu Leu Ile Gly Asp Tyr Ser Lys		
140	370	375	380
142	Ala Phe Leu Leu Gln Thr Val Asp Gly Lys His Gln Asp Leu Lys Tyr		
143	385	390	395
145	Ile Ser Pro Glu Thr Met Val Ala Leu Leu Thr Gly Lys Phe Ser Asn		400
146	405	410	415
148	Ile Val Asp Lys Phe Val Ile Val Asp Cys Arg Tyr Pro Tyr Glu Tyr		
149	420	425	430
151	Glu Gly Gly His Ile Lys Thr Ala Val Asn Leu Pro Leu Glu Arg Asp		
152	435	440	445
154	Ala Glu Ser Phe Leu Leu Lys Ser Pro Ile Ala Pro Cys Ser Leu Asp		
155	450	455	460
157	Lys Arg Val Ile Leu Ile Phe His Cys Glu Phe Ser Ser Glu Arg Gly		
158	465	470	475
160	Pro Arg Met Cys Arg Phe Ile Arg Glu Arg Asp Arg Ala Val Asn Asp		
161	485	490	495
163	Tyr Pro Ser Leu Tyr Tyr Pro Glu Met Tyr Ile Leu Lys Gly Gly Tyr		
164	500	505	510
166	Lys Glu Phe Phe Pro Gln His Pro Asn Phe Cys Glu Pro Gln Asp Tyr		
167	515	520	525
169	Arg Pro Met Asn His Glu Ala Phe Lys Asp Glu Leu Lys Thr Phe Arg		
170	530	535	540
172	Leu Lys Thr Arg Ser Trp Ala Gly Glu Arg Ser Arg Arg Glu Leu Cys		
173	545	550	555
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176	565		
179	<210> SEQ ID NO: 4		
180	<211> LENGTH: 539		
181	<212> TYPE: PRT		
182	<213> ORGANISM: Homo sapiens		
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186	<222> LOCATION: (312)		
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193	Ala Gly Val Cys Gly Gly Ala Gln Arg Pro Gly His Leu Pro Gly Leu		15
194	20	25	30
196	Leu Leu Gly Ser His Gly Leu Leu Gly Ser Pro Val Arg Ala Ala Ala		
197	35	40	45
199	Ser Ser Pro Val Thr Thr Leu Thr Gln Thr Met His Asp Leu Ala Gly		
200	50	55	60
202	Leu Gly Ser Glu Thr Pro Lys Ser Gln Val Gly Thr Leu Leu Phe Arg		
203	65	70	75
205	Ser Arg Ser Arg Leu Thr His Leu Ser Leu Ser Arg Arg Ala Ser Glu		80
206	85	90	95
208	Ser Ser Leu Ser Ser Glu Ser Ser Glu Ser Ser Asp Ala Gly Leu Cys		

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209	100	105	110
211	Met Asp Ser Pro Ser Pro Met Asp Pro His Met Ala Glu Gln Thr Phe		
212	115	120	125
214	Glu Gln Ala Ile Gln Ala Ala Ser Arg Ile Ile Arg Asn Glu Gln Phe		
215	130	135	140
217	Ala Ile Arg Arg Phe Gln Ser Met Pro Asp Gly Phe Val Phe Lys Met		
218	145	150	155
220	Pro Trp Lys Pro Thr His Pro Ser Ser Thr His Ala Leu Ala Glu Trp		
221	165	170	175
223	Ala Ser Arg Arg Glu Ala Phe Ala Gln Arg Pro Ser Ser Ala Pro Asp		
224	180	185	190
226	Leu Met Cys Leu Ser Pro Asp Arg Lys Met Glu Val Glu Glu Leu Ser		
227	195	200	205
229	Pro Leu Ala Leu Gly Arg Phe Ser Leu Thr Pro Ala Glu Gly Asp Thr		
230	210	215	220
232	Glu Glu Asp Asp Gly Phe Val Asp Ile Leu Glu Ser Asp Leu Lys Asp		
233	225	230	235
235	Asp Asp Ala Val Pro Pro Gly Met Glu Ser Leu Ile Ser Ala Pro Leu		
236	245	250	255
238	Val Lys Thr Leu Glu Lys Glu Glu Lys Asp Leu Val Met Tyr Ser		
239	260	265	270
241	Lys Cys Gln Arg Leu Phe Arg Ser Pro Ser Met Pro Cys Ser Val Ile		
242	275	280	285
244	Arg Pro Ile Leu Lys Arg Leu Glu Arg Pro Gln Asp Arg Asp Thr Pro		
245	290	295	300
247	Val Gln Asn Lys Arg Arg Ser Val Thr Pro Pro Glu Glu Gln Gln		
248	305	310	315
250	Glu Ala Glu Glu Pro Lys Ala Arg Val Leu Arg Ser Lys Ser Leu Cys		
251	325	330	335
253	His Asp Glu Ile Glu Asn Leu Leu Asp Ser Asp His Arg Glu Leu Ile		
254	340	345	350
256	Gly Asp Tyr Ser Lys Ala Phe Leu Leu Gln Thr Val Asp Gly Lys His		
257	355	360	365
259	Gln Asp Leu Lys Tyr Ile Ser Pro Glu Thr Met Val Ala Leu Leu Thr		
260	370	375	380
262	Gly Lys Phe Ser Asn Ile Val Asp Lys Phe Val Ile Val Asp Cys Arg		
263	385	390	395
265	Tyr Pro Tyr Glu Tyr Glu Gly Gly His Ile Lys Thr Ala Val Asn Leu		
266	405	410	415
268	Pro Leu Glu Arg Asp Ala Glu Ser Phe Leu Leu Lys Ser Pro Ile Ala		
269	420	425	430
271	Pro Cys Ser Leu Asp Lys Arg Val Ile Leu Ile Phe His Cys Glu Phe		
272	435	440	445
274	Ser Ser Glu Arg Gly Pro Arg Met Cys Arg Phe Ile Arg Glu Arg Asp		
275	450	455	460
277	Arg Ala Val Asn Asp Tyr Pro Ser Leu Tyr Tyr Pro Glu Met Tyr Ile		
278	465	470	475
280	Leu Lys Gly Gly Tyr Lys Glu Phe Phe Pro Gln His Pro Asn Phe Cys		
281	485	490	495

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283 Glu Pro Gln Asp Tyr Arg Pro Met Asn His Glu Ala Phe Lys Asp Glu
284 500 505 510
286 Leu Lys Thr Phe Arg Leu Lys Thr Arg Ser Trp Ala Gly Glu Arg Ser
287 515 520 525
289 Arg Arg Glu Leu Cys Ser Arg Leu Gln Asp Gln
290 530 535
293 <210> SEQ ID NO: 5
294 <211> LENGTH: 580
295 <212> TYPE: PRT
296 <213> ORGANISM: Homo sapiens
298 <220> FEATURE:
299 <221> NAME/KEY: MOD_RES
300 <222> LOCATION: (353)
301 <223> OTHER INFORMATION: PHOSPHORYLATION
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307 Ala Gly Val Cys Gly Gly Ala Gln Arg Pro Gly His Leu Pro Gly Leu
308 20 25 30
310 Leu Leu Gly Ser His Gly Leu Leu Gly Ser Pro Val Arg Ala Ala Ala
311 35 40 45
313 Ser Ser Pro Val Thr Thr Leu Thr Gln Thr Met His Asp Leu Ala Gly
314 50 55 60
316 Leu Gly Ser Glu Thr Pro Lys Ser Gln Val Gly Thr Leu Leu Phe Arg
317 65 70 75 80
319 Ser Arg Ser Arg Leu Thr His Leu Ser Leu Ser Arg Arg Ala Ser Glu
320 85 90 95
322 Ser Ser Leu Ser Ser Glu Ser Ser Glu Ser Ser Asp Ala Gly Leu Cys
323 100 105 110
325 Met Asp Ser Pro Ser Pro Met Asp Pro His Met Ala Glu Gln Thr Phe
326 115 120 125
328 Glu Gln Ala Ile Gln Ala Ala Ser Arg Ile Ile Arg Asn Glu Gln Phe
329 130 135 140
331 Ala Ile Arg Arg Phe Gln Ser Met Pro Val Arg Leu Leu Gly His Ser
332 145 150 155 160
334 Pro Val Leu Arg Asn Ile Thr Asn Ser Gln Ala Pro Asp Gly Arg Arg
335 165 170 175
337 Lys Ser Glu Ala Gly Ser Gly Ala Ala Ser Ser Ser Gly Glu Asp Lys
338 180 185 190
340 Glu Asn Asp Gly Phe Val Phe Lys Met Pro Trp Lys Pro Thr His Pro
341 195 200 205
343 Ser Ser Thr His Ala Leu Ala Glu Trp Ala Ser Arg Arg Glu Ala Phe
344 210 215 220
346 Ala Gln Arg Pro Ser Ser Ala Pro Asp Leu Met Cys Leu Ser Pro Asp
347 225 230 235 240
349 Arg Lys Met Glu Val Glu Glu Leu Ser Pro Leu Ala Leu Gly Arg Phe
350 245 250 255
352 Ser Leu Thr Pro Ala Glu Gly Asp Thr Glu Glu Asp Asp Gly Phe Val
353 260 265 270

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